

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

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- (i) APPLICANT: Hsei, Vanessa  
Koumenis, Iphigenia  
Leong, Steven R.  
Presta, Leonard G.  
Shahrokh, Zahra  
Zapata, Gerardo A.

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- (ii) TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
Humanized Anti-IL-8 Monoclonal Antibodies

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- (iii) NUMBER OF SEQUENCES: 76

- (iv) CORRESPONDENCE ADDRESS:

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- (A) ADDRESSEE: Genentech, Inc.  
(B) STREET: 1 DNA Way  
(C) CITY: South San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94080

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- (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WinPatin (Genentech)

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- (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:  
(B) FILING DATE: 20-Feb-1998  
(C) CLASSIFICATION:

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- (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Love, Richard B.  
(B) REGISTRATION NUMBER: 34,659  
(C) REFERENCE/DOCKET NUMBER: P1085R3PCT

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- (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 650/225-5530  
(B) TELEFAX: 650/952-9881

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- (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

55

CAGTCCAACT GTTCAGGACG CC 22

(2) INFORMATION FOR SEQ ID NO:2:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGCTGCTCA TGCTGTAGGT GC 22

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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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GAAGTTGATG TCTTGTGAGT GGC 23

(2) INFORMATION FOR SEQ ID NO:4:

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

40 GCATCCTAGA GTCACCGAGG AGCC 24

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

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50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CACTGGCTCA GGGAAATAAC CC 22

55 (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: Nucleic Acid  
    (C) STRANDEDNESS: Single  
5      (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

10      GGAGAGCTGG GAAGGTGTGC AC 22

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
15      (A) LENGTH: 35 base pairs  
        (B) TYPE: Nucleic Acid  
        (C) STRANDEDNESS: Single  
        (D) TOPOLOGY: Linear

20      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACAAACGCGT ACGCTGACAT CGTCATGACC CAGTC 35

25      (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 35 base pairs  
        (B) TYPE: Nucleic Acid  
30      (C) STRANDEDNESS: Single  
        (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

35      ACAAACGCGT ACGCTGATAT TGTCATGACT CAGTC 35

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
40      (A) LENGTH: 35 base pairs  
        (B) TYPE: Nucleic Acid  
        (C) STRANDEDNESS: Single  
        (D) TOPOLOGY: Linear

45      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACAAACGCGT ACGCTGACAT CGTCATGACA CAGTC 35

50      (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 37 base pairs  
55      (B) TYPE: Nucleic Acid  
        (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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GCTCTTCGAA TGGTGGGAAG ATGGATACAG TTGGTGC 37

(2) INFORMATION FOR SEQ ID NO:11:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGATGGGCCC GGATAGACCG ATGGGGCTGT TGT TTTGGC 39

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

25

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

30

CGATGGGCCC GGATAGACTG ATGGGGCTGT CGT TTTGGC 39

(2) INFORMATION FOR SEQ ID NO:13:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

40

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

45

CGATGGGCCC GGATAGACGG ATGGGGCTGT TGT TTTGGC 39

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 39 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGATGGGCCC GGATAGACAG ATGGGGCTGT TGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:15:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

10

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

15

CGATGGGCCC GGATAGACCG ATGGGGCTGT TGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:16:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGATGGGCCC GGATAGACTG ATGGGGCTGT TGTTTTGGC 39

30

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: Nucleic Acid

35

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

40

CGATGGGCCC GGATAGACAG ATGGGGCTGT TGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:18:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

55

CGATGGGCCC GGATAGACGG ATGGGGCTGT TGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

10 GACATTGTCA TGACACAGTC TCAAAAATTC ATGTCCACAT CAGTAGGAGA 50  
 CAGGGTCAGC GTCACCTGCA AGGCCAGTCA GAATGTGGGT ACTAATGTAG 100  
 15 CCTGGTATCA ACAGAAACCA GGGCAATCTC CTAAAGCACT GATTTACTCG 150  
 TCATCCTACC GGTACAGTGG AGTCCCTGAT CGCTTCACAG GCAGTGGATC 200  
 TGGGACAGAT TTCACTCTCA CCATCAGCCA TGTGCAGTCT GAAGACTTGG 250  
 20 CAGACTATTT CTGTCAGCAA TATAACATCT ATCCTCTCAC GTTCGGTCCT 300  
 GGGACCAAGC TGGAGTTGAA ACGGGCTGAT GCTGCACCAC CAACTGTATC 350  
 25 CATCTTCCCA CCATTCGAA 369

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

35 Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val  
     1                    5                    10                    15  
 40 Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly  
                     20                    25                    30  
   Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys  
                     35                    40                    45  
 45 Ala Leu Ile Tyr Ser Ser Ser Tyr Arg Tyr Ser Gly Val Pro Asp  
                     50                    55                    60  
   Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile  
                     65                    70                    75  
 50 Ser His Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln  
                     80                    85                    90  
 55 Tyr Asn Ile Tyr Pro Leu Thr Phe Gly Pro Gly Thr Lys Leu Glu  
                     95                    100                    105

Leu Lys Arg Ala Asp Ala Ala Pro Pro Thr Val Ser Ile Phe Pro  
 110 115 120

5 Pro Phe Glu  
 123

(2) INFORMATION FOR SEQ ID NO:21:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 417 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTCTATTGCT ACAAACGCGT ACGCTGAGGT GCAGCTGGTG GAGTCTGGGG 50  
 20 GAGGCTTAGT GCCGCCTGGA GGGTCCCTGA AACTCTCCTG TGCAGCCTCT 100  
 GGATTCATAT TCAGTAGTTA TGGCATGTCT TGGGTTCGCC AGACTCCAGG 150  
 CAAGAGCCTG GAGTTGGTCG CAACCATTAA TAATAATGGT GATAGCACCT 200  
 25 ATTATCCAGA CAGTGTGAAG GGCCGATTCA CCATCTCCCG AGACAATGCC 250  
 AAGAACACCC TGTACCTGCA AATGAGCAGT CTGAAGTCTG AGGACACAGC 300  
 30 CATGTTTTAC TGTGCAAGAG CCCTCATTAG TTCGGCTACT TGGTTTGTT 350  
 ACTGGGGCCA AGGGACTCTG GTCACTGTCT CTGCAGCCAA AACAACAGCC 400  
 CCATCTGTCT ATCCGGG 417

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(2) INFORMATION FOR SEQ ID NO:22:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 130 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

45 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Pro Pro Gly  
 1 5 10 15  
 Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser  
 20 25 30  
 50 Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Gly Lys Ser Leu  
 35 40 45  
 Glu Leu Val Ala Thr Ile Asn Asn Asn Gly Asp Ser Thr Tyr Tyr  
 55 50 55 60

Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala  
                                 65                                70                                75

5 Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp  
                                 80                                85                                90

Thr Ala Met Phe Tyr Cys Ala Arg Ala Leu Ile Ser Ser Ala Thr  
                                 95                                100                                105

10 Trp Phe Gly Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala  
                                 110                                115                                120

Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro  
                                 125                                130

15

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 base pairs  
 20 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:  
 25

ACAAACGCGT ACGCTGATAT CGTCATGACA G 31

(2) INFORMATION FOR SEQ ID NO:24:  
 30

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 35 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

40 GCAGCATCAG CTCTTCGAAG CTCCAGCTTG G 31

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 45 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:  
 50

CCACTAGTAC GCAAGTTCAC G 21

55 (2) INFORMATION FOR SEQ ID NO:26:



- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
5 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

10 GATGGGCCCT TGGTGGAGGC TGCAGAGACA GTG 33

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:  
15 (A) LENGTH: 714 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCT TTTTCTCTAT 50  
25 TGCTACAAAC GCGTACGCTG ATATCGTCAT GACACAGTCT CAAAAATTCA 100  
TGTCACATC AGTAGGAGAC AGGGTCAGCG TCACCTGCAA GGCCAGTCAG 150  
AATGTGGGTA CTAATGTAGC CTGGTATCAA CAGAAACCAG GGCAATCTCC 200  
30 TAAAGCACTG ATTTACTCGT CATCCTACCG GTACAGTGGA GTCCCTGATC 250  
GCTTCACAGG CAGTGGATCT GGGACAGATT TCACTCTCAC CATCAGCCAT 300  
35 GTGCAGTCTG AAGACTTGGC AGACTATTTT TGTCAGCAAT ATAACATCTA 350  
TCCTCTCACG TTCGGTCCCTG GGACCAAGCT GGAGCTTCGA AGAGCTGTGG 400  
CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAAATCT 450  
40 GGAAGTCTT CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC 500  
CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG 550  
45 AGAGTGTCAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC 600  
ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG 650  
CGAAGTCACC CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA 700  
50 GGGGAGAGTG TTAA 714

(2) INFORMATION FOR SEQ ID NO:28:

- 55 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 237 amino acids

(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

5	Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
10	Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	20	25	30	
	Gln	Lys	Phe	Met	Ser	Thr	Ser	Val	Gly	Asp	Arg	Val	Ser	Val	Thr	35	40	45	
15	Cys	Lys	Ala	Ser	Gln	Asn	Val	Gly	Thr	Asn	Val	Ala	Trp	Tyr	Gln	50	55	60	
	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Ala	Leu	Ile	Tyr	Ser	Ser	Ser	65	70	75	
20	Tyr	Arg	Tyr	Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	80	85	90	
	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	His	Val	Gln	Ser	Glu	Asp	95	100	105	
25	Leu	Ala	Asp	Tyr	Phe	Cys	Gln	Gln	Tyr	Asn	Ile	Tyr	Pro	Leu	Thr	110	115	120	
30	Phe	Gly	Pro	Gly	Thr	Lys	Leu	Glu	Leu	Arg	Arg	Ala	Val	Ala	Ala	125	130	135	
	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	140	145	150	
35	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	155	160	165	
40	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	170	175	180	
	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	185	190	195	
45	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	200	205	210	
	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	215	220	225	
50	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	230	235	237				

(2) INFORMATION FOR SEQ ID NO:29:

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

10 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT 50  
 TGCTACAAAC GCGTACGCTG AGGTGCAGCT GGTGGAGTCT GGGGGAGGCT 100  
 TAGTGCCGCC TGGAGGGTCC CTGAAACTCT CCTGTGCAGC CTCTGGATTG 150  
 15 ATATTTCAGTA GTTATGGCAT GTCTTGGGTT CGCCAGACTC CAGGCAAGAG 200  
 CCTGGAGTTG GTCGCAACCA TTAATAATAA TGGTGATAGC ACCTATTATC 250  
 CAGACAGTGT GAAGGGCCGA TTCACCATCT CCCGAGACAA TGCCAAGAAC 300  
 20 ACCCTGTACC TGCAAATGAG CAGTCTGAAG TCTGAGGACA CAGCCATGTT 350  
 TTA CTGTGCA AGAGCCCTCA TTAGTTCGGC TACTTGTTT GGTTACTGGG 400  
 25 GCCAAGGGAC TCTGGTCACT GTCTCTGCAG CCTCCACCAA GGGCCCATCG 450  
 GTCTTCCCCC TGGCACCCCTC CTCCAAGAGC ACCTCTGGGG GCACAGCGGC 500  
 CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCGGTG ACGGTGTCGT 550  
 30 GGAAGTCAGG CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCCTA 600  
 CAGTCCTCAG GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG 650  
 35 CAGCTTGGGC ACCCAGACCT ACATCTGCAA CGTGAATCAC AAGCCCAGCA 700  
 ACACCAAGGT GGACAAGAAA GTTGAGCCCA AATCTTGTGA CAAAACCTCAC 750  
 ACATGA 756

40

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 251 amino acids  
 45 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

50 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
     1                    5                    10                    15  
 Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser  
                     20                    25                    30  
 55 Gly Gly Gly Leu Val Pro Pro Gly Gly Ser Leu Lys Leu Ser Cys

	35	40	45
	Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr Gly Met Ser Trp Val		
	50	55	60
5	Arg Gln Thr Pro Gly Lys Ser Leu Glu Leu Val Ala Thr Ile Asn		
	65	70	75
	Asn Asn Gly Asp Ser Thr Tyr Tyr Pro Asp Ser Val Lys Gly Arg		
10	80	85	90
	Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln		
	95	100	105
15	Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Phe Tyr Cys Ala		
	110	115	120
	Arg Ala Leu Ile Ser Ser Ala Thr Trp Phe Gly Tyr Trp Gly Gln		
	125	130	135
20	Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser		
	140	145	150
	Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr		
25	155	160	165
	Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val		
	170	175	180
30	Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr		
	185	190	195
	Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser		
	200	205	210
35	Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile		
	215	220	225
	Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys		
40	230	235	240
	Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr		
	245	250 251	

45 (2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: Nucleic Acid

50 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

55

CAGTCCAACT GTTCAGGACG CC 22

## (2) INFORMATION FOR SEQ ID NO:32:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GTGCTGCTCA TGCTGTAGGT GC 22

## 15 (2) INFORMATION FOR SEQ ID NO:33:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

25

GAAGTTGATG TCTTGTGAGT GGC 23

## (2) INFORMATION FOR SEQ ID NO:34:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCATCCTAGA GTCACCGAGG AGCC 24

40

## (2) INFORMATION FOR SEQ ID NO:35:

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

50

CACTGGCTCA GGGAAATAAC CC 22

## (2) INFORMATION FOR SEQ ID NO:36:

55

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGAGAGCTGG GAAGGTGTGC AC 22

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(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

20

CCAATGCATA CGCTGACATC GTGATGACCC AGACCCC 37

(2) INFORMATION FOR SEQ ID NO:38:

25

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CCAATGCATA CGCTGATATT GTGATGACTC AGACTCC 37

35

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

45

CCAATGCATA CGCTGACATC GTGATGACAC AGACACC 37

(2) INFORMATION FOR SEQ ID NO:40:

50

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

5 AGATGTCAAT TGCTCACTGG ATGGTGGGAA GATGG 35

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 32 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CAAACGCGTA CGCTGAGATC CAGCTGCAGC AG 32

20 (2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: Nucleic Acid  
25 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

30

CAAACGCGTA CGCTGAGATT CAGCTCCAGC AG 32

(2) INFORMATION FOR SEQ ID NO:43:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGATGGGCCC GGATAGACCG ATGGGGCTGT TGTTTTGGC 39

45

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
50 (B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

55

CGATGGGCCC GGATAGACTG ATGGGGCTGT TGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:45:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGATGGGCCC GGATAGACAG ATGGGGCTGT TGTTTTGGC 39

15 (2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

25 CGATGGGCCC GGATAGACGG ATGGGGCTGT TGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:47:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 391 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

40 GATATCGTGA TGACACAGAC ACCACTCTCC CTGCCTGTCA GTCTTGAGAGA 50  
TCAGGCCTCC ATCTCTTGCA GATCTAGTCA GAGCCTTGTA CACGGTATTG 100  
GAAACACCTA TTTACATTGG TACCTGCAGA AGCCAGGCCA GTCTCCAAAG 150  
45 CTCCTGATCT ACAAAGTTTC CAACCGATTT TCTGGGGTCC CAGACAGGTT 200  
CAGTGGCAGT GGATCAGGGA CAGATTTTAC ACTCAGGATC AGCAGAGTGG 250  
50 AGGCTGAGGA TCTGGGACTT TATTTCTGCT CTCAAAGTAC ACATGTTCCG 300  
CTCACGTTTCG GTGCTGGGAC CAAGCTGGAG CTGAAACGGG CTGATGCTGC 350  
ACCAACTGTA TCCATCTTCC CACCATCCAG TGAGCAATTG A 391

55 (2) INFORMATION FOR SEQ ID NO:48:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu  
 1 5 10 15  
 Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val  
 20 25 30  
 His Gly Ile Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro  
 35 40 45  
 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe  
 50 55 60  
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
 65 70 75  
 Phe Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu  
 80 85 90  
 Tyr Phe Cys Ser Gln Ser Thr His Val Pro Leu Thr Phe Gly Ala  
 95 100 105  
 Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala Pro Thr Val  
 110 115 120  
 Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Lys  
 125 130 131

## (2) INFORMATION FOR SEQ ID NO:49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAGATTCAGC TGCAGCAGTC TGGACCTGAG CTGATGAAGC CTGGGGCTTC 50  
 AGTGAAGATA TCCTGCAAGG CTTCTGGTTA TTCATTCAGT AGCCACTACA 100  
 TGCCTGGGT GAAGCAGAGC CATGGAAAGA GCCTTGAGTG GATTGGCTAC 150  
 ATTGATCCTT CCAATGGTGA AACTACTTAC AACCAGAAAT TCAAGGGCAA 200  
 GGCCACATTG ACTGTAGACA CATCTTCCAG CACAGCCAAC GTGCATCTCA 250

GCAGCCTGAC ATCTGATGAC TCTGCAGTCT ATTTCTGTGC AAGAGGGGAC 300

TATAGATACA ACGGCGACTG GTTTTTCGAT GTCTGGGGNG NAGGGACCAC 350

5 GGTCACCGTC TCCTCCGCCA AAACCGACAG CCCCATCGGT CTATCCGGGC 400

CCATC 405

(2) INFORMATION FOR SEQ ID NO:50:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

20	Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly	15
	1 5 10	
	Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Ser	30
	20 25	
25	Ser His Tyr Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu	45
	35 40	
	Glu Trp Ile Gly Tyr Ile Asp Pro Ser Asn Gly Glu Thr Thr Tyr	60
	50 55	
30	Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser	75
	65 70	
	Ser Ser Thr Ala Asn Val His Leu Ser Ser Leu Thr Ser Asp Asp	90
	80 85	
35	Ser Ala Val Tyr Phe Cys Ala Arg Gly Asp Tyr Arg Tyr Asn Gly	105
	95 100	
	Asp Trp Phe Phe Asp Val Trp Gly Xaa Gly Thr Thr Val Thr Val	120
40	110 115	
	Ser Ser Ala Lys Thr Asp Ser Pro Ile Gly Leu Ser Gly Pro Ile	135
	125 130	

45 (2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: Nucleic Acid

50

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

55

CTTGGTGGAG GCGGAGGAGA CG 22

## (2) INFORMATION FOR SEQ ID NO:52:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GAAACGGGCT GTTGCTGCAC CAACTGTATT CATCTTCC 38

15 (2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: Nucleic Acid  
20 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

25 GTCACCGTCT CCTCCGCCTC CACCAAGGGC C 31

(2) INFORMATION FOR SEQ ID NO:54:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTTGGTGGAG GCGGAGGAGA CG 22

40

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 729 base pairs  
45 (B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

50

ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTTTCTAT 50

TGCTACAAAT GCATACGCTG ATATCGTGAT GACACAGACA CCACTCTCCC 100

55

TGCCTGTCAG TCTTGGAGAT CAGGCCTCCA TCTCTTGCAG ATCTAGTCAG 150

AGCCTTGTTAC ACGGTATTGG AAACACCTAT TTACATTGGT ACCTGCAGAA 200  
 GCCAGGCCAG TCTCCAAAGC TCCTGATCTA CAAAGTTTCC AACCGATTTT 250  
 5 CTGGGGTCCC AGACAGGTTC AGTGGCAGTG GATCAGGGAC AGATTTCACA 300  
 CTCAGGATCA GCAGAGTGGA GGCTGAGGAT CTGGGACTTT ATTTCTGCTC 350  
 10 TCAAAGTACA CATGTTCCGC TCACGTTCGG TGCTGGGACC AAGCTGGAGC 400  
 TGAAACGGGC TGTGCTGCA CCAACTGTAT TCATCTTCCC ACCATCCAGT 450  
 GAGCAATTGA AATCTGGAAC TGCCTCTGTT GTGTGCCTGC TGAATAACTT 500  
 15 CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550  
 CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600  
 20 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650  
 CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700  
 CAAAGAGCTT CAACAGGGGA GAGTGTTAA 729

25

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 242 amino acids  
 30 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

35 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
     1                    5                    10                    15  
 Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Val Met Thr Gln Thr  
                     20                    25                    30  
 40 Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser  
                     35                    40                    45  
 Cys Arg Ser Ser Gln Ser Leu Val His Gly Ile Gly Asn Thr Tyr  
 45                    50                    55                    60  
 Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu  
                     65                    70                    75  
 50 Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe  
                     80                    85                    90  
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile Ser Arg  
                     95                    100                    105  
 55 Val Glu Ala Glu Asp Leu Gly Leu Tyr Phe Cys Ser Gln Ser Thr

110 115 120  
 His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 125 130 135  
 5 Arg Ala Val Ala Ala Pro Thr Val Phe Ile Phe Pro Pro Ser Ser  
 140 145 150  
 10 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn  
 155 160 165  
 Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn  
 170 175 180  
 15 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
 185 190 195  
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser  
 200 205 210  
 20 Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr  
 215 220 225  
 His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
 230 235 240  
 25 Glu Cys  
 242

30 (2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 762 base pairs  
 (B) TYPE: Nucleic Acid  
 35 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

40 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTCTCTAT 50  
 TGCTACAAAC GCGTACGCTG AGATTCAGCT GCAGCAGTCT GGACCTGAGC 100  
 45 TGATGAAGCC TGGGGCTTCA GTGAAGATAT CCTGCAAGGC TTCTGGTTAT 150  
 TCATTGAGTA GCCACTACAT GCACTGGGTG AAGCAGAGCC ATGGAAAGAG 200  
 CCTTGAGTGG ATTGCTTACA TTGATCCTTC CAATGGTGAA ACTACTTACA 250  
 50 ACCAGAAATT CAAGGGCAAG GCCACATTGA CTGTAGACAC ATCTTCCAGC 300  
 ACAGCCAACG TGCATCTCAG CAGCCTGACA TCTGATGACT CTGCAGTCTA 350  
 55 TTTCTGTGCA AGAGGGGACT ATAGATACAA CGGCGACTGG TTTTTCGATG 400

TCTGGGGCGC AGGGACCACG GTCACCGTCT CCTCCGCCTC CACCAAGGGC 450  
 CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGCAC 500  
 5 AGCGGCCCTG GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG 550  
 TGTCGTGGAA CTCAGGCGCC CTGACCAGCG GCGTGACAC CTTCCCGGCT 600  
 GTCCTACAGT CCTCAGGACT CTACTCCCTC AGCAGCGTGG TGACCGTGCC 650  
 10 CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG AATCACAAGC 700  
 CCAGCAACAC CAAGGTGGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA 750  
 15 ACTCACACAT GA 762

## (2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:  
 20 (A) LENGTH: 253 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

25 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
 1 5 10 15  
 Ser Ile Ala Thr Asn Ala Tyr Ala Glu Ile Gln Leu Gln Gln Ser  
 30 20 25 30  
 Gly Pro Glu Leu Met Lys Pro Gly Ala Ser Val Lys Ile Ser Cys  
 35 35 40 45  
 Lys Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val  
 50 55 60  
 Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Tyr Ile Asp  
 40 65 70 75  
 Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Lys  
 80 85 90  
 Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Asn Val His  
 45 95 100 105  
 Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys Ala  
 110 115 120  
 Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp  
 50 125 130 135  
 Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
 140 145 150  
 55 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly

155 160 165  
 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
 170 175 180  
 5 Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val  
 185 190 195  
 10 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu  
 200 205 210  
 Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
 215 220 225  
 15 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
 230 235 240  
 Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
 245 250 253  
 20  
 (2) INFORMATION FOR SEQ ID NO:59:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 114 amino acids  
 25 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:  
 30 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu  
 1 5 10 15  
 Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val  
 20 25 30  
 35 His Gly Ile Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro  
 35 40 45  
 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Tyr Lys Val Ser Asn Arg  
 40 50 55 60  
 Phe Ser Gly Val Pro Asp Arg Phe Ser Asp Ser Gly Ser Gly Thr  
 65 70 75  
 45 Asp Phe Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Leu Gly  
 80 85 90  
 Leu Tyr Phe Cys Ser Gln Ser Thr His Val Pro Leu Thr Phe Gly  
 95 100 105  
 50 Ala Gly Thr Lys Lys Leu Glu Leu Lys Arg  
 110 114

(2) INFORMATION FOR SEQ ID NO:60:

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val
	1				5						10				15
10	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val
					20					25					30
	His	Gly	Ile	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro
					35					40					45
15	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Tyr	Lys	Val	Ser	Asn	Arg
					50					55					60
	Phe	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr
20					65					70					75
	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala
					80					85					90
25	Thr	Tyr	Tyr	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Leu	Thr	Phe	Gly
					95					100					105
	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg						
					110				114						

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 109 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

40	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val
	1				5					10					15
	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Lys	Thr	Ile	Ser
					20					25					30
45	Lys	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys
					35					40					45
	Leu	Leu	Ile	Tyr	Tyr	Ser	Gly	Ser	Thr	Leu	Glu	Ser	Gly	Val	Pro
					50					55					60
50	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr
					65					70					75
	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln
55					80					85					90



Gln His Asn Glu Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val  
                                   95                                  100                                  105

5 Glu Ile Lys Arg  
                                   109

(2) INFORMATION FOR SEQ ID NO:62:

10 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 117 amino acids  
       (B) TYPE: Amino Acid  
       (D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly  
   1                                  5                                  10                                  15

20 Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Ser  
                                   20                                  25                                  30

Ser His Tyr Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu  
                                   35                                  40                                  45

25 Glu Trp Ile Gly Tyr Ile Asp Pro Ser Asn Gly Glu Thr Thr Tyr  
                                   50                                  55                                  60

30 Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser  
                                   65                                  70                                  75

Ser Ser Thr Ala Asn Val His Leu Ser Ser Leu Thr Ser Asp Asp  
                                   80                                  85                                  90

35 Ser Ala Val Tyr Phe Cys Ala Ala Arg Gly Asp Tyr Arg Tyr Asn  
                                   95                                  100                                  105

Gly Asp Trp Phe Phe Asp Val Trp Gly Ala Gly Thr  
                                   110                                  115                                  117

40

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 117 amino acids  
       (B) TYPE: Amino Acid  
       (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

50 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly  
   1                                  5                                  10                                  15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Phe Ser  
                                   20                                  25                                  30

55 Ser His Tyr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu

		35		40		45
	Glu Trp Val Gly Tyr Ile Asp Pro Ser Asn Gly Glu Thr Thr Tyr					
		50		55		60
5	Asn Gln Lys Phe Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser					
		65		70		75
	Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp					
10		80		85		90
	Thr Ala Val Tyr Tyr Cys Ala Ala Arg Gly Asp Tyr Arg Tyr Asn					
		95		100		105
15	Gly Asp Trp Phe Phe Asp Val Trp Gly Gln Gly Thr					
		110		115		117

## (2) INFORMATION FOR SEQ ID NO:64:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 116 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

	Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly				
	1	5	10	15	
30	Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Thr				
		20	25	30	
	Gly His Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu				
		35	40	45	
35	Glu Trp Val Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Tyr				
		50	55	60	
	Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser				
40		65	70	75	
	Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp				
		80	85	90	
45	Thr Ala Val Tyr Tyr Cys Ala Ala Arg Gly Ile Tyr Phe Tyr Gly				
		95	100	105	
	Thr Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr				
		110	115	116	

50

## (2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 242 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

5 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
 1 5 10 15  
 Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser  
 20 25 30  
 10 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr  
 35 40 45  
 Cys Arg Ser Ser Gln Ser Leu Val His Gly Ile Gly Asn Thr Tyr  
 50 55 60  
 15 Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu  
 65 70 75  
 Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Ser Arg Phe  
 80 85 90  
 20 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser  
 95 100 105  
 25 Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ser Gln Ser Thr  
 110 115 120  
 His Val Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
 125 130 135  
 30 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 140 145 150  
 35 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn  
 155 160 165  
 Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn  
 170 175 180  
 40 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
 185 190 195  
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser  
 200 205 210  
 45 Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr  
 215 220 225  
 50 His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
 230 235 240  
 Glu Cys  
 242

55 (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
 1 5 10 15

Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Gln Ser  
 20 25 30

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys  
 35 40 45

Ala Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val  
 50 55 60

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Tyr Ile Asp  
 65 70 75

Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Arg  
 80 85 90

Phe Thr Leu Ser Arg Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln  
 95 100 105

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 110 115 120

Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp  
 125 130 135

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
 140 145 150

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 155 160 165

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
 170 175 180

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val  
 185 190 195

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu  
 200 205 210

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
 215 220 225

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
 230 235 240

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr

245

250

253

## (2) INFORMATION FOR SEQ ID NO:67:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 159 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met  
 1 5 10 15

Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn  
 20 25 30

Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr  
 35 40 45

20 Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly  
 50 55 60

Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Ser  
 25 65 70 75

Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu  
 80 85 90

30 Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val  
 95 100 105

Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe  
 110 115 120

35 Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala  
 125 130 135

Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe  
 40 140 145 150

Ala Asn Ile Leu Arg Asn Lys Glu Ser  
 155 159

## 45 (2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 780 base pairs  
 (B) TYPE: Nucleic Acid  
 50 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

55 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT 50

TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100  
 TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA 150  
 5 AGCTTAGTAC ATGGTATAGG TAACACGTAT TTACTCTGGT ATCAACAGAA 200  
 ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250  
 10 CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT 300  
 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350  
 ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400  
 15 TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450  
 GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500  
 20 CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550  
 CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACCC 600  
 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650  
 25 CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700  
 CAAAGAGCTT CAACAGGGGA GAGTGTTAAG CTGATCCTCT ACGCCGGACG 750  
 30 CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780

## (2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 242 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

40 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
 1 5 10 15  
 45 Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser  
 20 25 30  
 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr  
 35 40 45  
 50 Cys Arg Ser Ser Gln Ser Leu Val His Gly Ile Gly Asn Thr Tyr  
 50 55 60  
 Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu  
 65 70 75  
 55 Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Ser Arg Phe

80 85 90  
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser  
 95 100 105  
 5 Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ser Gln Ser Thr  
 110 115 120  
 10 His Val Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
 125 130 135  
 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 140 145 150  
 15 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn  
 155 160 165  
 Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn  
 170 175 180  
 20 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
 185 190 195  
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser  
 200 205 210  
 25 Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr  
 215 220 225  
 30 His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
 230 235 240  
 Glu Cys  
 242  
 35 (2) INFORMATION FOR SEQ ID NO:70:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 253 amino acids  
 40 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:  
 45 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
 1 5 10 15  
 Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser  
 20 25 30  
 50 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys  
 35 40 45  
 Ala Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val  
 55 50 55 60

Lys Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Tyr Ile Asp  
 65 70 75  
 Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Arg  
 5 80 85 90  
 Phe Thr Leu Ser Arg Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln  
 95 100 105  
 10 Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 110 115 120  
 Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp  
 125 130 135  
 15 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
 140 145 150  
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 20 155 160 165  
 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
 170 175 180  
 25 Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val  
 185 190 195  
 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu  
 200 205 210  
 30 Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
 215 220 225  
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
 35 230 235 240  
 Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
 245 250 253

40 (2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 amino acids

(B) TYPE: Amino Acid

45 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
 50 1 5 10 15  
 Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser  
 20 25 30  
 55 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr  
 35 40 45



Cys Arg Ser Ser Gln Ser Leu Val His Gly Ile Gly Ala Thr Tyr  
 50 55 60  
 5 Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu  
 65 70 75  
 Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Ser Arg Phe  
 80 85 90  
 10 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser  
 95 100 105  
 15 Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ser Gln Ser Thr  
 110 115 120  
 His Val Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
 125 130 135  
 20 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 140 145 150  
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn  
 155 160 165  
 25 Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn  
 170 175 180  
 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
 185 190 195  
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser  
 200 205 210  
 35 Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr  
 215 220 225  
 His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
 230 235 240  
 40 Glu Cys  
 242

## (2) INFORMATION FOR SEQ ID NO:72:

45

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 45 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Arg Met Lys  
 1 5 10 15  
 55 Gln Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His

20 25 30  
Leu Glu Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg  
35 40 45

5

## (2) INFORMATION FOR SEQ ID NO:73:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 780 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

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ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT 50  
TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100  
TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA 150  
AGCTTAGTAC ATGGTATAGG TGCTACGTAT TTACTTGGT ATCAACAGAA 200  
ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250  
CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT 300  
CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350  
ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400  
TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450  
GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500  
CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550  
CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600  
TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650  
CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700  
CAAAGAGCTT CAACAGGGGA GAGTGTTAAG CTGATCCTCT ACGCCGGACG 750  
CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780

50

## (2) INFORMATION FOR SEQ ID NO:74:

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 927 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

5 AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT 50  
 TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAC GCGTACGCTG 100  
 AGGTTTCAGCT AGTGCAGTCT GGCGGTGGCC TGGTGCAGCC AGGGGGCTCA 150  
 10 CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC TCCTTCTCGA GTCACATATAT 200  
 GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG GTTGGATATA 250  
 TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT 300  
 15 TTCACTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA 350  
 CAGCCTGCGT GCTGAGGACA CTGCCGTCTA TTACTGTGCA AGAGGGGATT 400  
 20 ATCGCTACAA TGGTGAAGTG TTCTTCGACG TCTGGGGTCA AGGAACCCTG 450  
 GTCACCGTCT CCTCGGCCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC 500  
 ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG 550  
 25 TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC 600  
 CTGACCAGCG GCGTGACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT 650  
 30 CTACTCCCTC AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC 700  
 AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTCGAC 750  
 AAGAAAGTTG AGCCCAAATC TTGTGACAAA ACTCACACAT GCCCCCGCTG 800  
 35 CCCAGCACCA GAACTGCTGG GCGGCCGCAT GAAACAGCTA GAGGACAAGG 850  
 TCGAAGAGCT ACTCTCCAAG AACTACCACC TAGAGAATGA AGTGGCAAGA 900  
 40 CTCAAAAAGC TTGTCGGGGA GCGCTAA 927

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:  
 45 (A) LENGTH: 298 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

50 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
     1                    5                    10                    15  
 55 Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Gln Ser  
                     20                    25                    30

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys  
 35 40 45  
 5 Ala Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val  
 50 55 60  
 Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Tyr Ile Asp  
 65 70 75  
 10 Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Arg  
 80 85 90  
 Phe Thr Leu Ser Arg Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln  
 95 100 105  
 15 Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 110 115 120  
 Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp  
 125 130 135  
 20 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
 140 145 150  
 25 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 155 160 165  
 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
 170 175 180  
 30 Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val  
 185 190 195  
 35 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu  
 200 205 210  
 Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
 215 220 225  
 40 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
 230 235 240  
 Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro  
 245 250 255  
 45 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Arg Met Lys Gln Leu  
 260 265 270  
 Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu  
 275 280 285  
 50 Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg  
 290 295 298

55 (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6563 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

10 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC 50  
TCATTGCTGA GTTGTATTAT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT 100  
GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT 150  
15 TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG 200  
GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCCTGA CGACGATACG 250  
20 GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA 300  
AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT 350  
ATAGTCGCTT TGTTTTTATT TTTAATGTA TTTGTAATA GAATTCGAGC 400  
25 TCGGTACCCG GGGATCCTCT CGAGGTTGAG GTGATTTTAT GAAAAAGAAT 450  
ATCGCATTTT TTCTTGCATC TATGTTTCGTT TTTTCTATTG CTACAAACGC 500  
30 ATACGCTGAT ATCCAGATGA CCCAGTCCCC GAGCTCCCTG TCCGCCTCTG 550  
TGGGCGATAG GGTCAACATC ACCTGCAGGT CAAGTCAAAG CTTAGTACAT 600  
GGTATAGGTG CTACGTATTT ACACTGGTAT CAACAGAAAC CAGGAAAAGC 650  
35 TCCGAAACTA CTGATTTACA AAGTATCCAA TCGATTCTCT GGAGTCCCTT 700  
CTCGCTTCTC TGGATCCGGT TCTGGGACGG ATTTCACTCT GACCATCAGC 750  
40 AGTCTGCAGC CAGAAGACTT CGCAACTTAT TACTGTTTAC AGAGTACTCA 800  
TGTCCCGCTC ACGTTTGGAC AGGGTACCAA GGTGGAGATC AAACGAACTG 850  
TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA 900  
45 TCTGGAAGTG CTTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA 950  
GGCCAAAGTA CAGTGAAGG TGGATAACGC CCTCCAATCG GGTAACCTCC 1000  
50 AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC 1050  
AGCACCTTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC 1100  
CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA 1150  
55 ACAGGGGAGA GTGTTAAGCT GATCCTCTAC GCCGGACGCA TCGTGGCCCT 1200

AGTACGCAAC TAGTCGTAAA AAGGGTATCT AGAGGTTGAG GTGATTTTAT 1250  
GAAAAAGAAT ATCGCATTTT TTCTTGCATC TATGTTCGTT TTTTCTATTG 1300  
5 CTACAAACGC GTACGCTGAG GTTCAGCTAG TGCAGTCTGG CGGTGGCCTG 1350  
GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT CTGGCTACTC 1400  
10 CTTCTCGAGT CACTATATGC ACTGGGTCCG TCAGGCCCCG GGTAAGGGCC 1450  
TGAATGGGT TGGATATATT GATCCTTCCA ATGGTGAAAC TACGTATAAT 1500  
CAAAAGTTCA AGGGCCGTTT CACTTTATCT CGCGACAACT CCAAAAACAC 1550  
15 AGCATACCTG CAGATGAACA GCCTGCGTGC TGAGGACACT GCCGTCTATT 1600  
ACTGTGCAAG AGGGGATTAT CGCTACAATG GTGACTGGTT CTTGACGTC 1650  
20 TGGGGTCAAG GAACCCTGGT CACCGTCTCC TCGGCCTCCA CCAAGGGCCC 1700  
ATCGGTCTTC CCCCTGGCAC CCTCCTCCAA GAGCACCTCT GGGGGCACAG 1750  
CGGCCCTGGG CTGCCTGGTC AAGGACTACT TCCCCGAACC GGTGACGGTG 1800  
25 TCGTGGAAC CAGGCGCCCT GACCAGCGGC GTGCACACCT TCCCGGCTGT 1850  
CCTACAGTCC TCAGGACTCT ACTCCCTCAG CAGCGTGGTG ACCGTGCCCT 1900  
30 CCAGCAGCTT GGGCACCCAG ACCTACATCT GCAACGTGAA TCACAAGCCC 1950  
AGCAACACCA AGGTCGACAA GAAAGTTGAG CCCAAATCTT GTGACAAAAC 2000  
TCACACATGC CCGCCGTGCC CAGCACCAGA ACTGCTGGGC GGCCGCATGA 2050  
35 AACAGCTAGA GGACAAGGTC GAAGAGCTAC TCTCCAAGAA CTACCACCTA 2100  
GAGAATGAAG TGGCAAGACT CAAAAGCTT GTCGGGGAGC GCTAAGCATG 2150  
40 CGACGGCCCT AGAGTCCCTA ACGCTCGGTT GCCGCCGGGC GTTTTTTATT 2200  
GTAACTCAT GTTTGACAGC TTATCATCGA TAAGCTTTAA TGCGGTAGTT 2250  
TATCACAGTT AAATTGCTAA CGCAGTCAGG CACCGTGTAT GAAATCTAAC 2300  
45 AATGCGCTCA TCGTCATCCT CGGCACCGTC ACCCTGGATG CTGTAGGCAT 2350  
AGGCTTGGTT ATGCCGGTAC TGCCGGGCCT CTTGCGGGAT ATCGTCCATT 2400  
50 CCGACAGCAT CGCCAGTCAC TATGGCGTGC TGCTAGCGCT ATATGCGTTG 2450  
ATGCAATTTT TATGCGCACC CGTTCTCGGA GCACTGTCCG ACCGCTTTGG 2500  
CCGCCGCCCA GTCCTGCTCG CTTGCTACT TGGAGCCACT ATCGACTACG 2550  
55 CGATCATGGC GACCACACCC GTCCTGTGGA TCCTCTACGC CGGACGCATC 2600

GTGGCCGGCA TCACCGGCGC CACAGGTGCG GTTGCTGGCG CCTATATCGC 2650  
 CGACATCACC GATGGGGAAG ATCGGGCTCG CCACTTCGGG CTCATGAGCG 2700  
 5 CTTGTTTCGG CGTGGGTATG GTGGCAGGCC CCGTGGCCGG GGGACTGTTG 2750  
 GGCGCCATCT CCTTGACGC ACCATTCTT GCGGCGGCGG TGCTCAACGG 2800  
 10 CCTCAACCTA CTAAGGGCT GCTTCCTAAT GCAGGAGTCG CATAAGGGAG 2850  
 AGCGTCGTCC GATGCCCTTG AGAGCCTTCA ACCCAGTCAG CTCCTTCCGG 2900  
 TGGGCGCGGG GCATGACTAT CGTCGCCGCA CTTATGACTG TCTTCTTTAT 2950  
 15 CATGCAACTC GTAGGACAGG TGCCGGCAGC GCTCTGGGTC ATTTTCGGCG 3000  
 AGGACCGCTT TCGCTGGAGC GCGACGATGA TCGGCCTGTC GCTTGCGGTA 3050  
 20 TTCGGAATCT TGCACGCCCT CGCTCAAGCC TTCGTCACTG GTCCCGCCAC 3100  
 CAAACGTTTC GGCGAGAAGC AGGCCATTAT CGCCGGCATG GCGGCCGACG 3150  
 CGCTGGGCTA CGTCTTGCTG GCGTTCGCGA CGCGAGGCTG GATGGCCTTC 3200  
 25 CCCATTATGA TTCTTCTCGC TTCCGGCGGC ATCGGGATGC CCGCGTTGCA 3250  
 GGCCATGCTG TCCAGGCAGG TAGATGACGA CCATCAGGGA CAGCTTCAAG 3300  
 30 GATCGCTCGC GGCTCTTACC AGCCTAACTT CGATCACTGG ACCGCTGATC 3350  
 GTCACGGCGA TTTATGCCGC CTCGGCGAGC ACATGGAACG GGTGCGCATG 3400  
 GATTGTAGGC GCCGCCCTAT ACCTTGCTG CCTCCCCGCG TTGCGTCGCG 3450  
 35 GTGCATGGAG CCGGGCCACC TCGACCTGAA TGAAGCCGG CGGCACCTCG 3500  
 CTAACGGATT CACCACTCCA AGAATTGGAG CCAATCAATT CTTGCGGAGA 3550  
 40 ACTGTGAATG CGCAAACCAA CCCTTGGCAG AACATATCCA TCGCGTCCGC 3600  
 CATCTCCAGC AGCCGCACGC GCGCATCTC GGGCAGCGTT GGGTCCTGGC 3650  
 CACGGGTGCG CATGATCGTG CTCCTGTCGT TGAGGACCCG GCTAGGCTGG 3700  
 45 CGGGGTTGCC TTAAGGTTA GCAGAATGAA TCACCGATAC GCGAGCGAAC 3750  
 GTGAAGCGAC TGCTGCTGCA AAACGTCTGC GACCTGAGCA ACAACATGAA 3800  
 50 TGGTCTTCGG TTTCCGTGTT TCGTAAAGTC TGGAAACGCG GAAGTCAGCG 3850  
 CCCTGCACCA TTATGTTCCG GATCTGCATC GCAGGATGCT GCTGGCTACC 3900  
 CTGTGGAACA CCTACATCTG TATTAACGAA GCGCTGGCAT TGACCCTGAG 3950  
 55 TGATTTTCT CTGGTCCCGC CGCATCCATA CCGCCAGTTG TTTACCCTCA 4000

CAACGTTCCA GTAACCGGGC ATGTTTCATCA TCAGTAACCC GTATCGTGAG 4050  
CATCCTCTCT CGTTTCATCG GTATCATTAC CCCCATGAAC AGAAATTCCC 4100  
5 CCTTACACGG AGGCATCAAG TGACCAAACA GGAAAAAACC GCCCTTAACA 4150  
TGGCCCCTT TATCAGAAGC CAGACATTAA CGCTTCTGGA GAAACTCAAC 4200  
10 GAGCTGGACG CGGATGAACA GGCAGACATC TGTGAATCGC TTCACGACCA 4250  
CGCTGATGAG CTTTACCGCA GCTGCCTCGC GCGTTTCGGT GATGACGGTG 4300  
AAAACCTCTG ACACATGCAG CTCCCGGAGA CGGTCACAGC TTGTCTGTAA 4350  
15 GCGGATGCCG GGAGCAGACA AGCCCGTCAG GCGCGTCAG CGGGTGTGG 4400  
CGGGTGTGCG GGCGCAGCCA TGACCCAGTC ACGTAGCGAT AGCGGAGTGT 4450  
20 ATACTGGCTT AACTATGCGG CATCAGAGCA GATTGTACTG AGAGTGCACC 4500  
ATATGCGGTG TGAAATACCG CACAGATGCG TAAGGAGAAA ATACCGCATC 4550  
AGGCGCTCTT CCGCTTCCTC GCTCACTGAC TCGCTGCGCT CGGTCGTTTCG 4600  
25 GCTGCGGCGA GCGGTATCAG CTCACTCAA GGCGGTAATA CGGTTATCCA 4650  
CAGAATCAGG GGATAACGCA GGAAAGAACA TGTGAGCAAA AGGCCAGCAA 4700  
30 AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG CTGGCGTTTT TCCATAGGCT 4750  
CCGCCCCCTT GACGAGCATC AAAAAATCG ACGCTCAAGT CAGAGGTGGC 4800  
GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC TGGAAGCTCC 4850  
35 CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT ACCTGTCCGC 4900  
CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC TCATAGCTCA CGCTGTAGGT 4950  
40 ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG TGTGCACGAA 5000  
CCCCCGTTC AGCCCGACCG CTGCGCCTTA TCCGGTAACT ATCGTCTTGA 5050  
GTCCAACCCG GTAAGACACG ACTTATCGCC ACTGGCAGCA GCCACTGGTA 5100  
45 ACAGGATTAG CAGAGCGAGG TATGTAGGCG GTGCTACAGA GTTCTTGAAG 5150  
TGGTGGCCTA ACTACGGCTA CACTAGAAGG ACAGTATTTG GTATCTGCGC 5200  
50 TCTGCTGAAG CCAGTTACCT TCGGAAAAAG AGTTGGTAGC TCTTGATCCG 5250  
GCAAACAAAC CACCGCTGGT AGCGGTGGTT TTTTGTGTTG CAAGCAGCAG 5300  
ATTACGCGCA GAAAAAAGG ATCTCAAGAA GATCCTTTGA TCTTTTCTAC 5350  
55 GGGGTCTGAC GCTCAGTGGA ACGAAACTC ACGTTAAGGG ATTTTGGTCA 5400



5450 TGAGATTATC AAAAAGGATC TTCACCTAGA TCCTTTTAAA TTAAAAATGA  
5500 AGTTTTAAAT CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA  
5550 CCAATGCTTA ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTCGTT  
5600 CATCCATAGT TGCCTGACTC CCCGTCGTGT AGATAACTAC GATACGGGAG  
5650 GGCTTACCAT CTGGCCCCAG TGCTGCAATG ATACCGCGAG ACCCAGCTC  
5700 ACCGGCTCCA GATTTATCAG CAATAAACCA GCCAGCCGGA AGGGCCGAGC  
5750 GCAGAAGTGG TCCTGCAACT TTATCCGCCT CCATCCAGTC TATTAATTGT  
5800 TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT  
5850 TGTTGCCATT GCTGCAGGCA TCGTGGTGTG ACGCTCGTCG TTTGGTATGG  
5900 CTTCAATCAG CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC  
5950 ATGTTGTGCA AAAAAGCGGT TAGCTCCTTC GGTCTCCGA TCGTTGTCAG  
6000 AAGTAAGTTG GCCGCAGTGT TATCACTCAT GGTTATGGCA GCACTGCATA  
6050 ATTCTCTTAC TGTCATGCCA TCCGTAAGAT GCTTTTCTGT GACTGGTGAG  
6100 TACTCAACCA AGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC  
6150 TTGCCC GGCG TCAACACGGG ATAATACCGC GCCACATAGC AGAACTTTAA  
6200 AAGTGCTCAT CATTGGA AAA CGTTCTTCGG GGCGAAA ACT CTCAAGGATC  
6250 TTACCGCTGT TGAGATCCAG TTCGATGTAA CCCACTCGTG CACCCA ACTG  
6300 ATCTTCAGCA TCTTTTACTT TCACCAGCGT TTCTGGGTGA GCAAAAACAG  
6350 GAAGGCAAAA TGCCGCAAAA AAGGGAATAA GGGCGACACG GAAATGTTGA  
6400 ATACTCATAC TCTTCCTTTT TCAATATTAT TGAAGCATTT ATCAGGGTTA  
6450 TTGTCTCATG AGCGGATACA TATTTGAATG TATTTAGAAA AATAAACAAA  
6500 TAGGGGTTCC GCGCACATTT CCCC GAAAAG TGCCACCTGA CGTCTAAGAA  
6550 ACCATTATTA TCATGACATT AACCTATAAA AATAGGCGTA TCACGAGGCC  
CTTTCGTCTT CAA 6563